

APR 07 2003

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/632,722

DATE: 04/02/2003

TIME: 12:19:46

Input Set : A:\-57.app

Output Set: N:\CRF4\04022003\I632722.raw

3 <110> APPLICANT: Himmelspach, Michele
 4 Schlokat, Uwe
 5 Baxter Aktiengesellschaft
 7 <120> TITLE OF INVENTION: Factor X Analog With an Improved Ability to be
 8 Activated
 10 <130> FILE REFERENCE: 20695C-005700US
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/632,722
 13 <141> CURRENT FILING DATE: 2000-08-04
 15 <150> PRIOR APPLICATION NUMBER: AT A1377/99
 16 <151> PRIOR FILING DATE: 1999-08-10
 18 <160> NUMBER OF SEQ ID NOS: 18
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1467
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1467)
 30 <223> OTHER INFORMATION: factor X
 32 <400> SEQUENCE: 1
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 34 Met Gly Arg Pro Leu His Leu Val Leu Ser Ala Ser Leu Ala Gly
 35 1 5 10 15
 37 ctg ctg ctg ctc ggg gaa agt ctg ttc atc cgc agg gag cag gcc aac 96
 38 Leu Leu Leu Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn
 39 20 25 30
 41 aac atc ctg gcg agg gtc acg agg gcc aat tcc ttt ctt gaa gag atg 144
 42 Asn Ile Leu Ala Arg Val Thr Arg Ala Asn Ser Phe Leu Glu Glu Met
 43 35 40 45
 45 aag aaa gga cac ctc gaa aga gag tgc atg gaa gag acc tgc tca tac 192
 46 Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr Cys Ser Tyr
 47 50 55 60
 49 gaa gag gcc cgc gag gtc ttt gag gac agc gac aag acg aat gaa ttc 240
 50 Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe
 51 65 70 75 80
 53 tgg aat aaa tac aaa gat ggc gac cag tgt gag acc agt cct tgc cag 288
 54 Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln
 55 85 90 95
 57 aac cag ggc aaa tgt aaa gac ggc ctc ggg gaa tac acc tgc acc tgt 336
 58 Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu Tyr Thr Cys Thr Cys
 59 100 105 110
 61 tta gaa gga ttc gaa ggc aaa aac tgt gaa tta ttc aca cgg aag ctc 384

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62 Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu
63      115      120      125
65 tgc agc ctg gac aac ggg gac tgt gac cag ttc tgc cac gag gaa cag 432
66 Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln
67      130      135      140
69 aac tct gtg gtg tgc tcc tgc gcc cgc ggg tac acc ctg gct gac aac 480
70 Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn
71 145      150      155      160
73 ggc aag gcc tgc att ccc aca ggg ccc tac ccc tgt ggg aaa cag acc 528
74 Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr
75      165      170      175
77 ctg gaa cgc agg aag agg tca gtg gcc cag gcc acc agc agc agc ggg 576
78 Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly
79      180      185      190
81 gag gcc cct gac agc atc aca tgg aag cca tat gat gca gcc gac ctg 624
82 Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
83      195      200      205
85 gac ccc acc gag aac ccc ttc gac ctg ctt gac ttc aac cag acg cag 672
86 Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln
87      210      215      220
89 cct gag agg ggc gac aac aac ctc acc agg atc gtg gga ggc cag gaa 720
90 Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu
91 225      230      235      240
93 tgc aag gac ggg gag tgt ccc tgg cag gcc ctg ctc atc aat gag gaa 768
94 Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu
95      245      250      255
97 aac gag ggt ttc tgt ggt gga act att ctg agc gag ttc tac atc cta 816
98 Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu
99      260      265      270
101 acg gca gcc cac tgt ctc tac caa gcc aag aga ttc aag gtg agg gta 864
102 Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val
103      275      280      285
105 ggg gac cgg aac acg gag cag gag gag ggc ggt gag gcg gtg cac gag 912
106 Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu
107      290      295      300
109 gtg gag gtg gtc atc aag cac aac cgg ttc aca aag gag acc tat gac 960
110 Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp
111 305      310      315      320
113 ttc gac atc gcc gtg ctc cgg ctc aag acc ccc atc acc ttc cgc atg 1008
114 Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met
115      325      330      335
117 aac gtg gcg cct gcc tgc ctc ccc gag cgt gac tgg gcc gag tcc acg 1056
118 Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr
119      340      345      350
121 ctg atg acg cag aag acg ggg att gtg agc ggc ttc ggg cgc acc cac 1104
122 Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His
123      355      360      365
125 gag aag ggc cgg cag tcc acc agg ctc aag atg ctg gag gtg ccc tac 1152
126 Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr

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127      370      375      380
129 gtg gac cgc aac agc tgc aag ctg tcc agc agc ttc atc atc acc cag 1200
130 Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Phe Ile Ile Thr Gln
131 385      390      395      400
133 aac atg ttc tgt gcc ggc tac gac acc aag cag gag gat gcc tgc cag 1248
134 Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln
135      405      410      415
137 ggg gac agc ggg ggc ccg cac gtc acc cgc ttc aag gac acc tac ttc 1296
138 Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe
139      420      425      430
141 gtg aca ggc atc gtc agc tgg gga gag agc tgt gcc cgt aag ggg aag 1344
142 Val Thr Gly Ile Val Ser Trp Gly Glu Ser Cys Ala Arg Lys Gly Lys
143      435      440      445
145 tac ggg atc tac acc aag gtc acc gcc ttc ctc aag tgg atc gac agg 1392
146 Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg
147      450      455      460
149 tcc atg aaa acc agg ggc ttg ccc aag gcc aag agc cat gcc ccg gag 1440
150 Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu
151 465      470      475      480
153 gtc ata acg tcc tct cca tta aag tga 1467
154 Val Ile Thr Ser Ser Pro Leu Lys
155      485
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 488
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <223> OTHER INFORMATION: factor X
166 <400> SEQUENCE: 2
167 Met Gly Arg Pro Leu His Leu Val Leu Leu Ser Ala Ser Leu Ala Gly
168 1      5      10      15
169 Leu Leu Leu Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn
170      20      25      30
171 Asn Ile Leu Ala Arg Val Thr Arg Ala Asn Ser Phe Leu Glu Glu Met
172      35      40      45
173 Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr Cys Ser Tyr
174      50      55      60
175 Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe
176 65      70      75      80
177 Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln
178      85      90      95
179 Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu Tyr Thr Cys Thr Cys
180      100      105      110
181 Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu
182      115      120      125
183 Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln
184      130      135      140
185 Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn
186 145      150      155      160

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187 Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr
188                               165 170 175
189 Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly
190                               180 185 190
191 Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
192                               195 200 205
193 Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln
194                               210 215 220
195 Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu
196 225                               230 235 240
197 Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu
198                               245 250 255
199 Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu
200                               260 265 270
201 Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val
202                               275 280 285
203 Gly Asp Arg Asn Thr Glu Gln Glu Gly Gly Glu Ala Val His Glu
204                               290 295 300
205 Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp
206 305                               310 315 320
207 Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met
208                               325 330 335
209 Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr
210                               340 345 350
211 Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His
212                               355 360 365
213 Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr
214                               370 375 380
215 Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln
216 385                               390 395 400
217 Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln
218                               405 410 415
219 Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe
220                               420 425 430
221 Val Thr Gly Ile Val Ser Trp Gly Glu Ser Cys Ala Arg Lys Gly Lys
222                               435 440 445
223 Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg
224                               450 455 460
225 Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu
226 465                               470 475 480
227 Val Ile Thr Ser Ser Pro Leu Lys
228                               485
231 <210> SEQ ID NO: 3
232 <211> LENGTH: 34
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR 5' primer
238 oligonucleotide #2911

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240 <400> SEQUENCE: 3
241 attactcgag aagcttacca tggggcgccc actg 34
244 <210> SEQ ID NO: 4
245 <211> LENGTH: 24
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR 3' primer
251     oligonucleotide #2912
253 <400> SEQUENCE: 4
254 attacaattg ctgcagggat ccac 24
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 21
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR 5' primer
264     oligonucleotide #4211
266 <400> SEQUENCE: 5
267 ggcaaggcct gcattccac a 21
270 <210> SEQ ID NO: 6
271 <211> LENGTH: 55
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR 3' primer
277     oligonucleotide #5039
279 <400> SEQUENCE: 6
280 gcgctccac gatcctggtg aagtcattaa agctttgctc aggctgcgtc tggtt 55
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284 <211> LENGTH: 12
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence:factor IX
290     protease cutting site in the region of the
291     activation peptide
293 <400> SEQUENCE: 7
294 Gln Ser Phe Asn Asp Phe Thr Arg Val Val Gly Gly
295 1 5 10
298 <210> SEQ ID NO: 8
299 <211> LENGTH: 12
300 <212> TYPE: PRT
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence:factor X
305     protease cutting site in the region of the
306     activation peptide
308 <400> SEQUENCE: 8

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/632,722

DATE: 04/02/2003

TIME: 12:19:47

Input Set : A:\-57.app

Output Set: N:\CRF4\04022003\I632722.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number